SEQUENCE LISTING

<110> Kordyum, Vitaliy A.
Chernykh, Svitlana I.
Slavchenko, Iryna Yu.
Vozianov, Oleksandr

<120> PHAGE-DEPENDENT SUPER PRODUCTION OF
BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES

<130> PHAGE.006A

<150> 09/318,288
<151> 1999-05-25

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> This sequence was chemically synthesized based
upon the amino acid sequence of human acidic
fibroblast growth factor (155 amino acids) using
codons which are used in highly expressed proteins
from E. coli.

<221> CDS
<222> (122)...(590)

<400> 1
gcgtagagga tcgagatctc gatcccgcga aattaatacg actcactata ggggaattgt 60
gagcggataa caattcccct ctagaaataa ttttgtttaa ctttaagaag gagatataca 120
t atg gct gaa ggg gaa atc acc acc ttt aca gcg tta acg gag aaa ttt 169
Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
1 5 10 15

aac ctt ccg ccc ggg aat tac aaa aaa ccc aag ctt ctt tac tgc agt 217
Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
20 25 30

aac gga gga cac ttc ctg cga att ctg cca gat ggc aca gta gat ggg 265
Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
35 40 45

act cgc gat cgc tcc gac cag cac att cag ctg caa ctc tcg gcc gaa 313
Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
50 55 60

agc gtt gga gag gtc tat atc aag tcg acg gag act ggc cag tac ctt 361
Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu

```
 65                  70                  75                  80

gcc atg gac acc gat ggg ctt ctg tat ggc tca cag acg cct aac gaa   409
Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
                85                  90                  95

gaa tgc ttg ttt cta gaa aga cta gaa gaa aac cat tac aac acg tac   457
Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
            100                 105                 110

ata tcg aaa aaa cat gca gag aag aac tgg ttt gta ggc ctt aaa aaa   505
Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
        115                 120                 125

aat ggt tcc tgt aag cgt gga cca cgg act cac tat ggc caa aag gct   553
Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
    130                 135                 140

atc ttg ttc ctg cca cta cca gtg agc tcc gac taa g gatccgaatt      600
Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp  *
145                 150                 155

cgagctccgt cgacaagctt gcggccgcac                                 630

<210> 2
<211> 155
<212> PRT
<213> Homo sapiens

<400> 2
Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
 1               5                  10                  15
Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
            20                  25                  30
Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
        35                  40                  45
Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
    50                  55                  60
Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
65                  70                  75                  80
Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
                85                  90                  95
Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
            100                 105                 110
Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
        115                 120                 125
Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
    130                 135                 140
Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
145                 150                 155


<210> 3
<211> 468
<212> DNA
<213> Homo sapiens
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<400> 3
atggctgaag gggaaatcac caccttcaca gccctgaccg agaagtttaa tctgcctcca 60
gggaattaca agaagcccaa actcctctac tgtagcaacg ggggccactt cctgaggatc 120
cttccggatg gcacagtgga tgggacaagg gacaggagcg accagcacat tcagctgcag 180
ctcagtgcgg aaagcgtggg ggaggtgtat ataaagagta ccgagactgg ccagtacttg 240
gccatggaca ccgacgggct tttatacggc tcacagacac caaatgagga atgtttgttc 300
ctggaaaggc tggaggagaa ccattacaac acctatatat ccaagaagca tgcagagaag 360
aattggtttg ttggcctcaa gaagaatggg agctgcaaac gcggtcctcg gactcactat 420
ggccagaaag caatcttgtt tctccccctg ccagtctctt ctgattaa 468

<210> 4
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> This sequence is a chemically synthesized sequence
encoding a 134 amino acid form of fibroblast
growth factor with alterations for preferred codon
usage in E. coli

<221> CDS
<222> (122)...(526)

<400> 4
gcgtagagga tcgagatctc gatcccgcga aattaatacg actcactata ggggaattgt 60
gagcggataa caattcccct ctagaaataa ttttgtttaa ctttaagaag gagatataca 120
t atg aat tac aaa aaa ccc aag ctt ctt tac tgc agt aac gga gga cac 169
Met Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His
1 5 10 15

ttc ctg cga att ctg cca gat ggc aca gta gat ggg act cgc gat cgc 217
Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly Thr Arg Asp Arg
20 25 30

tcc gac cag cac att cag ctg caa ctc tcg gcc gaa agc gtt gga gag 265
Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu Ser Val Gly Glu
35 40 45

gtc tat atc aag tcg acg gag act ggc cag tac ctt gcc atg gac acc 313
Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp Thr
50 55 60

gat ggg ctt ctg tat ggc tca cag acg cct aac gaa gaa tgc ttg ttt 361
Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu Phe
65 70 75 80

cta gaa aga cta gaa gaa aac cat tac aac acg tac ata tcg aaa aaa 409
Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys
85 90 95

cat gca gag aag aac tgg ttt gta ggc ctt aaa aaa aat ggt tcc tgt 457
His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys
100 105 110

aag cgt gga cca cgg act cac tat ggc caa aag gct atc ttg ttc ctg 505
Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu

```
        115                 120                 125

cca cta cca gtg agc tcc gac taaggatccg aattcgagct ccgtcgacaa      556
Pro Leu Pro Val Ser Ser Asp
    130                 135

gcttgcggcc gcactcgagc accaccacca ccaccactga gatccggctg ctaacaaagc 616
ccgaaaggaa gctg                                                   630

<210> 5
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<223> Translated protein sequence for the chemically
      synthesized 134 amino acid form of fibroblast
      growth factor

<400> 5
Met Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His
 1               5                  10                  15
Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly Thr Arg Asp Arg
            20                  25                  30
Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu Ser Val Gly Glu
        35                  40                  45
Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp Thr
    50                  55                  60
Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu Phe
65                  70                  75                  80
Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys
                85                  90                  95
His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys
            100                 105                 110
Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu
        115                 120                 125
Pro Leu Pro Val Ser Ser Asp
    130                 135


<210> 6
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> This sequence is a chemically synthesized sequence
      encoding a 140 amino acid form of fibroblast
      growth factor with alterations for preferred codon
      usage in E. coli

<221> CDS
<222> (122)...(544)

<400> 6
gcgtagagga tcgagatctc gatcccgcga aattaatacg actcactata ggggaattgt 60
gagcggataa caattcccct ctagaaataa ttttgtttaa ctttaagaag gagatataca 120
```

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t atg ttt aac ctt ccg ccc ggg aat tac aaa aaa ccc aag ctt ctt tac 169
  Met Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
   1               5                  10                  15

tgc agt aac gga gga cac ttc ctg cga att ctg cca gat ggc aca gta   217
Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
             20                  25                  30

gat ggg act cgc gat cgc tcc gac cag cac att cag ctg caa ctc tcg   265
Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
         35                  40                  45

gcc gaa agc gtt gga gag gtc tat atc aag tcg acg gag act ggc cag   313
Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
     50                  55                  60

tac ctt gcc atg gac acc gat ggg ctt ctg tat ggc tca cag acg cct   361
Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
 65                  70                  75                  80

aac gaa gaa tgc ttg ttt cta gaa aga cta gaa gaa aac cat tac aac   409
Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
                 85                  90                  95

acg tac ata tcg aaa aaa cat gca gag aag aac tgg ttt gta ggc ctt   457
Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
            100                 105                 110

aaa aaa aat ggt tcc tgt aag cgt gga cca cgg act cac tat ggc caa   505
Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
        115                 120                 125

aag gct atc ttg ttc ctg cca cta cca gtg agc tcc gac taaggatccg    554
Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
    130                 135                 140

aattcgagct ccgtcgacaa gcttgcggcc gcactcgagc accaccacca ccaccactga 614
gatccggctg ctaaca                                                 630
```

<210> 7
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<223> Translated protein sequence for the chemically synthesized 140 amino acid form of fibroblast growth factor

<400> 7

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Met Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
 1               5                  10                  15
Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
            20                  25                  30
Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
        35                  40                  45
Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
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```
    50                  55                  60
Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
65                  70                  75                  80
Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
                85                  90                  95
Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
            100                 105                 110
Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
        115                 120                 125
Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
    130                 135                 140
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<210> 8
<211> 1822
<212> DNA
<213> Artificial Sequence

<220>
<221> TATA_signal
<222> (102)...(107)

<221> CDS
<222> (193)...(202)

<221> intron
<222> (203)...(458)

<221> CDS
<222> (459)...(619)

<221> intron
<222> (620)...(828)

<221> CDS
<222> (829)...(948)

<221> intron
<222> (949)...(1041)

<221> CDS
<222> (1042)...(1206)

<221> intron
<222> (1207)...(1459)

<221> CDS
<222> (1460)...(1654)

<223> Chemically synthesized sequence for Human Growth Hormone using codons preferred for expression in E. coli

<400> 8
ggagcttcta aattatccat tagcacaagc ccgtcagtgg ccccatgcat aaatgtacac 60
agaaacaggt gggggcaaca gtgggagaga aggggccagg gtataaaaag ggcccacaag 120
agaccggctc aaggatccca aggcccaact ccccgaacca ctcagggtcc tgtggacgct 180

```
cacctagctg ca atg gct aca g gtaagcgccc ctaaaatccc tttgggcaca      232
             Met Ala Thr
              1

atgtgtcctg aggggagagg cagcgacctg tagatgggac gggggcacta accctcaggt 292
ttggggcttc tgaatgagta tcgccatgta agcccagtat ggccaatctc agaaagctcc 352
tggtccctgg agggatggag agagaaaaac aaacagctcc tggagcaggg agagtgctgg 412
cctcttgctc tccggctccc tctgttgccc tctggtttct ccccag gc tcc cgg acg 469
                                                    Gly Ser Arg Thr
                                                         5

tcc ctg ctc ctg gct ttt ggc ctg ctc tgc ctg ccc tgg ctt caa gag   517
Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu
         10                  15                  20

ggc agt gcc ttc cca acc att ccc tta tcc agg ctt ttt gac aac gct   565
Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala
     25                  30                  35

atg ctc cgc gcc cat cgt ctg cac cag ctg gcc ttt gac acc tac cag   613
Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln
 40                  45                  50                  55

gag ttt gtaagctctt ggggaatggg tgcgcatcag gggtggcagg aaggggtgac    669
Glu Phe


tttccccccgc tgggaaataa gaggaggaga ctaaggagct cagggttttt cccgaagcga 729
aaatgcaggc agatgagcac acgctgagtg aggttcccag aaaagtaaca atgggagctg 789
gtctccagcg tagaccttgg tgggcggtcc ttctcctag gaa gaa gcc tat atc    843
                                        Glu Glu Ala Tyr Ile
                                                60

cca aag gaa cag aag tat tca ttc ctg cag aac ccc cag acc tcc ctc   891
Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu
         65                  70                  75

tgt ttc tca gag tct att ccg aca ccc tcc aac agg gag gaa aca caa   939
Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln
     80                  85                  90

cag aaa tcc gtgagtggat gccttgaccc caggcgggga tgggggagac           988
Gln Lys Ser
 95

ctgtagtcag agcccccggg cagcacaggc caatgcccgt ccttcccctg cag aac    1044
                                                        Asn


cta gag ctg ctc cgc atc tcc ctg ctg ctc atc cag tcg tgg ctg gag   1092
Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu
    100                 105                 110

ccc gtg cag ttc ctc agg agt gtc ttc gcc aac agc ctg gtg tac ggc   1140
Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly
115                 120                 125                 130
```

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gcc tct gac agc aac gtc tat gac ctc cta aag gac cta gag gaa ggc   1188
Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly
                135                 140                 145

atc caa acg ctg atg ggg gtgggggtgg cgctaggggt ccccaatctt         1236
Ile Gln Thr Leu Met Gly
            150

ggagccccac tgactttgag agctgtgtta gagaaacact gctgccctct ttttagcagt 1296
ccaggccctg acccaagaga actcacctta ttcttcattt ccccctcgtga atcctctagc 1356
ctttctctac accctgaagg ggagggagga aaatgaatga atgagaaagg gagggagcag 1416
tacccaagcg cttggcctct ccttctcttc cttcactttg cag agg ctg gaa gat   1471
                                              Arg Leu Glu Asp
                                                  155

ggc agc ccc cgg act ggg cag atc ttc aag cag acc tac agc aag ttc   1519
Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe
            160                 165                 170

gac aca aac tca cac aac gat gac gca cta ctc aag aac tac ggg ctg   1567
Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu
        175                 180                 185

ctc tac tgc ttc agg aag gac atg gac aag gtc gag aca ttc ctg cgc   1615
Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg
    190                 195                 200

atc gtg cag tgc cgc tct gtg gag ggc agc tgt ggc ttc tagctgcccg    1664
Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
205                 210                 215

ggtggcatcc ctgtgacccc tccccagtgc ctctcctggc cttggaagtt gccactccag 1724
tgcccaccag ccttgtccta ataaaattaa gttgcatcat tttgtctgac taggtgtcct 1784
ctataatatt atggggtgga ggggggtggt ttggagca                         1822
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<210> 9
<211> 217
<212> PRT
<213> Homo sapiens

<400> 9

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Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
 1               5                  10                  15
Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
            20                  25                  30
Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
        35                  40                  45
Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
    50                  55                  60
Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65                  70                  75                  80
Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
                85                  90                  95
Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
            100                 105                 110
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
        115                 120                 125
```

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
130 135 140
Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
145 150 155 160
Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
165 170 175
His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
180 185 190
Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
195 200 205
Arg Ser Val Glu Gly Ser Cys Gly Phe
210 215

<210> 10
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized sequence for human
interferon alpha- 2b

<221> promoter
<222> (231)...(249)

<221> CDS
<222> (320)...(784)

<400> 10
gggcgctgac ttccgcgttt ccagacttta cgaaacacgg aaaccgaaga ccattcatgt 60
tgttgctcag gtcgcagacg ttttgcagca gcagtcgctt cacgttcgct cgcgtatcgg 120
tgattcattc tgctaaccag taaggcaacc ccgccagcct agccgggtcc tcaacgacag 180
gagcacgatc atgcgcaccc gtggggccgc cagatctcga tcccgcgaaa ttaatacgac 240
tcactatagg ggaattgtga gcggataaca attcccctct agaaataatt ttgtttaact 300
ttaagaagga gatatacat atg gct gaa ggg gaa atc acc acc ttt aca gcg 352
Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala
1 5 10

tta acg gag aaa ttt aac ctt ccg ccc ggg aat tac aaa aaa ccc aag 400
Leu Thr Glu Lys Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys
15 20 25

ctt ctt tac tgc agt aac gga gga cac ttc ctg cga att ctg cca gat 448
Leu Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp
30 35 40

ggc aca gta gat ggg act cgc gat cgc tcc gac cag cac att cag ctg 496
Gly Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu
45 50 55

caa ctc tcg gcc gaa agc gtt gga gag gtc tat atc aag tcg acg gag 544
Gln Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu
60 65 70 75

act ggc cag tac ctt gcc atg gac acc gat ggg ctt ctg tat ggc tca 592
Thr Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser

```
                80                  85                  90

cag acg cct aac gaa gaa tgc ttg ttt cta gaa aga cta gaa gaa aac   640
Gln Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn
            95                  100                 105

cat tac aac acg tac ata tcg aaa aaa cat gca gag aag aac tgg ttt   688
His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe
        110                 115                 120

gta ggc ctt aaa aaa aat ggt tcc tgt aag cgt gga cca cgg act cac   736
Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His
    125                 130                 135

tat ggc caa aag gct atc ttg ttc ctg cca cta cca gtg agc tcc gac   784
Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
140                 145                 150                 155

taaggatccg aattcgagct ccgtcgacaa gcttgcggcc gcactcgagc accaccacca 844
ccaccactga gatccggctg ctaacaaagc ccgaaaggaa gctgagttgg ctgctgccac 904
cgctgagcaa taactagcat aacccccttgg ggcctctaaa cgggtcttga ggggtttttt 964
gctgaaagga ggaactatat ccggat                                      990

<210> 11
<211> 155
<212> PRT
<213> Homo sapiens

<220>
<223> Translated protein sequence for the chemically
      synthesized human interferon alpha-2b

<400> 11
Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
 1               5                  10                  15
Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
            20                  25                  30
Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
        35                  40                  45
Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
    50                  55                  60
Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
65                  70                  75                  80
Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
                85                  90                  95
Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
            100                 105                 110
Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
        115                 120                 125
Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
    130                 135                 140
Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
145                 150                 155
```